

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/540,634
Source: P4710
Date Processed by STIC: 7/7/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 07/07/2005

PATENT APPLICATION: US/10/540,634

TIME: 09:46:02

Input Set : N:\DA\PTO.DA.txt

Output Set: N:\CRF4\07072005\J540634.raw

4 <110> APPLICANT: DE WILDE, Gert Jules Hector

6 <120> TITLE OF INVENTION: KINASE SEQUENCES USEFUL FOR DEVELOPING COMPOUNDS FOR THE PREVENTION

7 AND/OR TREATMENT OF METABOLIC DISEASES AND NUCLEOTIDE SEQUENCES ENCODING SUCH

8 KINASE SEQUENCES

10 <130> FILE REFERENCE: D0590.70034US01

C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/540,634

C--> 13 <141> CURRENT FILING DATE: 2005-06-23

15 <150> PRIOR APPLICATION NUMBER: GB 0230014.3

16 <151> PRIOR FILING DATE: 2003-12-23

18 <150> PRIOR APPLICATION NUMBER: US 60/436,380

19 <151> PRIOR FILING DATE: 2003-12-23

21 <160> NUMBER OF SEQ ID NOS: 13

23 <170> SOFTWARE: PatentIn version 3.1

25 <210> SEQ ID NO: 1

26 <211> LENGTH: 2949

27 <212> TYPE: DNA

28 <213> ORGANISM: Caenorhabditis elegans

30 <400> SEQUENCE: 1

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33 ttcagtaata aggatccaga gcagagatat caagatttaa gagaaattgg acatggatct 120

35 tttggagctg tctattttgc atatgacaaa aaaaatgagc agactgttgc gattaaaaag 180

37 atgaatttta gtggaaaaca ggctgtcgaa aaatggaatg atattcttaa agaagtgtct 240

39 tttctgaata cagttgttca tccacatatt gtcgactaca aggccttggt tcttaaggac 300

41 actacatggt ggcttgtgat ggagtactgt attggctctg cagccgatat agtggatgtc 360

43 ttgcgaaaag gaatgcgaga agtcgaaatc gctgcgattt gctctcaaac tttggatgct 420

45 cttcgatata ttcactctct gaagcgaata catcgagata ttaaagctgg aaatattctg 480

47 ctatctgatc atgctattgt taaactagct gatttcggat ccgcatccct ggtagatccg 540

49 gctcaaaactt tcatcggaac gccgtttttc atggccccag aggtaattct ggcaatggat 600

51 gagggtcact acacggatcg tgcagatatt tggtcattgg gtatcacgtg tatagagctg 660

53 gccgaacgtc gtccaccatt gttcagtatg aatgcaatgt ctgccctcta ccatattgct 720

55 caaaatgatc ctccaactct ttctccaatt gacactagcg aacaaccgga atggctcgctg 780

57 gaattcgctt aatttataga caaatgtctt cgaaaaccag cagaagagcg aatgtcagct 840

59 gaagaatgct ttcgacatcc attcattcaa cggctctcgcc catcagacac aattcaggaa 900

61 ctcatcaga gaacgaaaaa tatgggatta gagttggata attttcaata caaaaagatg 960

63 agaaaactca tgtattttga tgaaacagaa ggaaaagaag gaagtgaagg aaatggagca 1020

65 tctgatgatt tagattttca tggaaatgaa gctaattcaa ttggaagagc aggagattct 1080

67 gcgtcatctc gaagtgcctt tcttacttct ttccgatcaa tgcagagtag tggaggagct 1140

69 ggtcttttag tgtccaccaa tacgacgggt gctatggata atgtgcatgg atcctctgga 1200

71 tacggtaatg gaagtgttc gacgacgagc tccgcacgcc gccgtcctcc aattccttcg 1260

73 caaatgcctc cttctacatc aacgtctggt ttggaacta tgccgagtca tggatcagtt 1320

75 ggagcatcga ttacggcgat cgcagtcagt ccaacaccgt ctccctcaga acctatccca 1380

77 acatcacaaac caacatcgaa atcagaatca tcttctatac tcgaaactgc acacgatgat 1440

79 cctttggaca cgtcgatacg tgctccagtg aaagacttgc atatgccgca tcgagcagtc 1500

P.6

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81 aaggaacgaa tagccacgtt gcaaaatcac aaattcgcca cgcttcgttc ccagagaata 1560
83 atcaatcagg aacaagaaga atatacgaaa gagaacaata tgtatgagca aatgagcaag 1620
85 tacaagcatc tacgacaagc acatcacaaa gagctccaac aatttgaaga acgatgtgca 1680
87 ttagatagag agcaactgcg tgtgaaaatg gatcgagaac tcgaacaatt gacaacgaca 1740
89 tactcgaaaag aaaagatgag agtgaggtgt tcacagaata atgaactaga caaacggaaa 1800
91 aaagatatcg aagatgggga gaaaaagatg aaaaagacga aaaatagtca aaatcagcag 1860
93 cagatgaaac tgtattcagc gcaacaattg aaagaataca agtataacaa ggaggcacag 1920
95 aaaacacgat tacgaagtct gaacatgcct cgaagtactt atgagaacgc aatgaaagaa 1980
97 gtgaaagccg atctgaatcg agtgaaagat gcacgggaaa atgattttga cgagaagctt 2040
99 cgtgcagaac ttgaagatga aattgtaagg tatcgaggc aacaactcag taatcttcat 2100
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111 caagtttgtga agactcagac tcgccaattt aagctctacc ttacacaaat ggtgcaagta 2460
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117 gtgaagctcg agtcgtggca agaagatgaa caacgggttc ttagtgagaa gttggagaaa 2640
119 gaattggaag aattgattgc ttatcagaag aagacgagag ccacattaga agagcagatt 2700
121 aaaaaggaac gtacggcact cgaagaacga attggcacac gacgtgcaat gcttgaacag 2760
123 aagattattg aagaacgcga acaaattggga gaaatgcgtc gactaaagaa ggagcaaadc 2820
125 cgtgatcgac acagtcaaga acgccaatcg ctcgagaatc atttcgtacg gacgggctcg 2880
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132 <210> SEQ ID NO: 2

133 <211> LENGTH: 982

134 <212> TYPE: PRT

135 <213> ORGANISM: Caenorhabditis elegans

137 <400> SEQUENCE: 2

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144 20 25 30
147 Leu Arg Glu Ile Gly His Gly Ser Phe Gly Ala Val Tyr Phe Ala Tyr
148 35 40 45
151 Asp Lys Lys Asn Glu Gln Thr Val Ala Ile Lys Lys Met Asn Phe Ser
152 50 55 60
155 Gly Lys Gln Ala Val Glu Lys Trp Asn Asp Ile Leu Lys Glu Val Ser
156 65 70 75 80
159 Phe Leu Asn Thr Val Val His Pro His Ile Val Asp Tyr Lys Ala Cys
160 85 90 95
163 Phe Leu Lys Asp Thr Thr Cys Trp Leu Val Met Glu Tyr Cys Ile Gly
164 100 105 110
167 Ser Ala Ala Asp Ile Val Asp Val Leu Arg Lys Gly Met Arg Glu Val
168 115 120 125
171 Glu Ile Ala Ala Ile Cys Ser Gln Thr Leu Asp Ala Leu Arg Tyr Leu
172 130 135 140
175 His Ser Leu Lys Arg Ile His Arg Asp Ile Lys Ala Gly Asn Ile Leu

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176 145          150          155          160
179 Leu Ser Asp His Ala Ile Val Lys Leu Ala Asp Phe Gly Ser Ala Ser
180          165          170          175
183 Leu Val Asp Pro Ala Gln Thr Phe Ile Gly Thr Pro Phe Phe Met Ala
184          180          185          190
187 Pro Glu Val Ile Leu Ala Met Asp Glu Gly His Tyr Thr Asp Arg Ala
188          195          200          205
191 Asp Ile Trp Ser Leu Gly Ile Thr Cys Ile Glu Leu Ala Glu Arg Arg
192          210          215          220
195 Pro Pro Leu Phe Ser Met Asn Ala Met Ser Ala Leu Tyr His Ile Ala
196 225          230          235          240
199 Gln Asn Asp Pro Pro Thr Leu Ser Pro Ile Asp Thr Ser Glu Gln Pro
200          245          250          255
203 Glu Trp Ser Leu Glu Phe Val Gln Phe Ile Asp Lys Cys Leu Arg Lys
204          260          265          270
207 Pro Ala Glu Glu Arg Met Ser Ala Glu Glu Cys Phe Arg His Pro Phe
208          275          280          285
211 Ile Gln Arg Ser Arg Pro Ser Asp Thr Ile Gln Glu Leu Ile Gln Arg
212          290          295          300
215 Thr Lys Asn Met Val Leu Glu Leu Asp Asn Phe Gln Tyr Lys Lys Met
216 305          310          315          320
219 Arg Lys Leu Met Tyr Leu Asp Glu Thr Glu Gly Lys Glu Gly Ser Glu
220          325          330          335
223 Gly Asn Gly Ala Ser Asp Asp Leu Asp Phe His Gly Asn Glu Ala Asn
224          340          345          350
227 Ser Ile Gly Arg Ala Gly Asp Ser Ala Ser Ser Arg Ser Ala Ser Leu
228          355          360          365
231 Thr Ser Phe Arg Ser Met Gln Ser Ser Gly Gly Ala Gly Leu Leu Val
232          370          375          380
235 Ser Thr Asn Thr Thr Gly Ala Met Asp Asn Val His Gly Ser Ser Gly
236 385          390          395          400
239 Tyr Gly Asn Gly Ser Ser Ser Thr Thr Ser Ser Ala Arg Arg Arg Pro
240          405          410          415
243 Pro Ile Pro Ser Gln Met Leu Ser Ser Thr Ser Thr Ser Gly Val Gly
244          420          425          430
247 Thr Met Pro Ser His Gly Ser Val Gly Ala Ser Ile Thr Ala Ile Ala
248          435          440          445
251 Val Asn Pro Thr Pro Ser Pro Ser Glu Pro Ile Pro Thr Ser Gln Pro
252          450          455          460
255 Thr Ser Lys Ser Glu Ser Ser Ser Ile Leu Glu Thr Ala His Asp Asp
256 465          470          475          480
259 Pro Leu Asp Thr Ser Ile Arg Ala Pro Val Lys Asp Leu His Met Pro
260          485          490          495
263 His Arg Ala Val Lys Glu Arg Ile Ala Thr Leu Gln Asn His Lys Phe
264          500          505          510
267 Ala Thr Leu Arg Ser Gln Arg Ile Ile Asn Gln Glu Gln Glu Glu Tyr
268          515          520          525
271 Thr Lys Glu Asn Asn Met Tyr Glu Gln Met Ser Lys Tyr Lys His Leu
272          530          535          540

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275 Arg Gln Ala His His Lys Glu Leu Gln Gln Phe Glu Glu Arg Cys Ala
276 545 550 555 560
279 Leu Asp Arg Glu Gln Leu Arg Val Lys Met Asp Arg Glu Leu Glu Gln
280 565 570 575
283 Leu Thr Thr Thr Tyr Ser Lys Glu Lys Met Arg Val Arg Cys Ser Gln
284 580 585 590
287 Asn Asn Glu Leu Asp Lys Arg Lys Lys Asp Ile Glu Asp Gly Glu Lys
288 595 600 605
291 Lys Met Lys Lys Thr Lys Asn Ser Gln Asn Gln Gln Gln Met Lys Leu
292 610 615 620
295 Tyr Ser Ala Gln Gln Leu Lys Glu Tyr Lys Tyr Asn Lys Glu Ala Gln
296 625 630 635 640
299 Lys Thr Arg Leu Arg Ser Leu Asn Met Pro Arg Ser Thr Tyr Glu Asn
300 645 650 655
303 Ala Met Lys Glu Val Lys Ala Asp Leu Asn Arg Val Lys Asp Ala Arg
304 660 665 670
307 Glu Asn Asp Phe Asp Glu Lys Leu Arg Ala Glu Leu Glu Asp Glu Ile
308 675 680 685
311 Val Arg Tyr Arg Arg Gln Gln Leu Ser Asn Leu His Gln Leu Glu Glu
312 690 695 700
315 Gln Leu Asp Asp Glu Asp Val Asn Val Gln Glu Arg Gln Met Asp Thr
316 705 710 715 720
319 Arg His Gly Leu Leu Ser Lys Gln His Glu Met Thr Arg Asp Leu Glu
320 725 730 735
323 Ile Gln His Leu Asn Glu Leu His Ala Met Lys Lys Arg His Leu Glu
324 740 745 750
327 Thr Gln His Glu Ala Glu Ser Ala Ser Gln Asn Glu Tyr Thr Gln Arg
328 755 760 765
331 Gln Gln Asp Glu Leu Arg Lys Lys His Ala Met Gln Ser Arg Gln Gln
332 770 775 780
335 Pro Arg Asp Leu Lys Ile Gln Glu Ala Gln Ile Arg Lys Gln Tyr Arg
336 785 790 795 800
339 Gln Val Val Lys Thr Gln Thr Arg Gln Phe Lys Leu Tyr Leu Thr Gln
340 805 810 815
343 Met Val Gln Val Val Pro Lys Asp Glu Gln Lys Glu Leu Thr Ser Arg
344 820 825 830
347 Leu Lys Gln Asp Gln Met Gln Lys Val Ala Leu Leu Ala Ser Gln Tyr
348 835 840 845
351 Glu Ser Gln Ile Lys Lys Met Val Gln Asp Lys Thr Val Lys Leu Glu
352 850 855 860
355 Ser Trp Gln Glu Asp Glu Gln Arg Val Leu Ser Glu Lys Leu Glu Lys
356 865 870 875 880
359 Glu Leu Glu Glu Leu Ile Ala Tyr Gln Lys Lys Thr Arg Ala Thr Leu
360 885 890 895
363 Glu Glu Gln Ile Lys Lys Glu Arg Thr Ala Leu Glu Glu Arg Ile Gly
364 900 905 910
367 Thr Arg Arg Ala Met Leu Glu Gln Lys Ile Ile Glu Glu Arg Glu Gln
368 915 920 925
371 Met Gly Glu Met Arg Arg Leu Lys Lys Glu Gln Ile Arg Asp Arg His

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Input Set : N:\DA\PTO.DA.txt

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384      980
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388 <211> LENGTH: 4188
389 <212> TYPE: DNA
390 <213> ORGANISM: Homo sapiens
392 <300> PUBLICATION INFORMATION:
393 <308> DATABASE ACCESSION NO: genbank NM_016281
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408 aggggtgctg aaggaccag agattgccga tctattctac aaagatgatc ctgaggaact 360
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412 tgctcacacc aatgaggtgg tggcaattaa gaagatgtcc tatagtggga agcagaccca 480
414 tgagaaatgg caagatattc ttaaggaagt taaattttta cgacaattga agcatcctaa 540
416 tactattgag taaaaggct gttacttgaa agaacacact gcttggttgg tgatggaata 600
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434 ggaaaggcca acatcagcag aactattaag gcatgacttt gttcgacgag accggccact 1140
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RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 72,3245,3263,3278

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:60
M:341 Repeated in SeqNo=9